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RAW SEQUENCE LISTING

DATE: 10/15/2004

PATENT APPLICATION: US/10/658,884

TIME: 12:39:31

Input Set : N:\CrF4\Refhold\10_folder\J658884.raw

Output Set: N:\CRF4\10152004\J658884.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:

- 2 (i) APPLICANT: Bandman, Olga
- 3 Goli, Surya K.
- 4 (ii) TITLE OF INVENTION: NOVEL HUMAN MAGE-LIKE PROTEIN
- 5 (iii) NUMBER OF SEQUENCES: 6
- 6 (iv) CORRESPONDENCE ADDRESS:
- 7 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
- 8 (B) STREET: 3174 Porter Drive
- 9 (C) CITY: Palo Alto
- 10 (D) STATE: CA
- 11 (E) COUNTRY: USA
- 12 (F) ZIP: 94304

13 (v) COMPUTER READABLE FORM:

- 14 (A) MEDIUM TYPE: Diskette
- 15 (B) COMPUTER: IBM Compatible
- 16 (C) OPERATING SYSTEM: DOS
- 17 (D) SOFTWARE: FastSEQ for Windows Version 2.0

18 (vi) CURRENT APPLICATION DATA:

- 19 (A) APPLICATION NUMBER: US/10/658,884
- 20 (B) FILING DATE: 09-Sep-2003
- 21 (C) CLASSIFICATION: 435

22 (vii) PRIOR APPLICATION DATA:

- 23 (A) APPLICATION NUMBER: US/08/773,870
- 24 (B) FILING DATE: 27-DEC-1996

25 (viii) ATTORNEY/AGENT INFORMATION:

- 26 (A) NAME: Billings, Lucy J.
- 27 (B) REGISTRATION NUMBER: 36,749
- 28 (C) REFERENCE/DOCKET NUMBER: PF-0179 US

29 (ix) TELECOMMUNICATION INFORMATION:

- 30 (A) TELEPHONE: 415-855-0555
- 31 (B) TELEFAX: 415-845-4166
- 32 (C) TELEX:

33 (2) INFORMATION FOR SEQ ID NO: 1:

34 (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 411 amino acids
- 36 (B) TYPE: amino acid
- 37 (C) STRANDEDNESS: single
- 38 (D) TOPOLOGY: linear

39 (vii) IMMEDIATE SOURCE:

- 40 (A) LIBRARY: Consensus
- 41 (B) CLONE: Consensus

42 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ENTERED

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W--> 43 Met Ala Phe Pro Arg Pro Lys Lys Asn Leu Pro Gln Pro Lys Xaa Ala
      44 1 5 10 15
      45 Ala Thr Glu Gly Pro Ser Ala Ala Ser Gly Val Pro Gln Thr Gly Pro
      46 20 25 30
      47 Gly Arg Glu Val Ala Ala Thr Arg Pro Lys Thr Thr Lys Ser Gly Lys
      48 35 40 45
      49 Ala Leu Ala Lys Thr Arg Trp Val Glu Pro Gln Asn Val Val Ala Ala
      50 50 55 60
      51 Ala Ala Ala Lys Ala Lys Met Ala Thr Ser Ile Pro Glu Pro Glu Gly
      52 65 70 75 80
      53 Ala Ala Ala Ala Thr Ala Gln His Ser Ala Glu Pro Trp Ala Arg Met
      54 85 90 95
      55 Gly Gly Lys Arg Thr Lys Lys Ser Lys His Leu Asp Asp Glu Tyr Glu
      56 100 105 110
      57 Ser Ser Glu Glu Glu Arg Glu Thr Pro Ala Val Pro Pro Thr Trp Arg
      58 115 120 125
      59 Ala Ser Gln Pro Ser Leu Thr Val Arg Ala Gln Leu Ala Pro Arg Pro
      60 130 135 140
      61 Pro Met Ala Pro Arg Ser Gln Ile Pro Ser Arg His Val Leu Cys Leu
      62 145 150 155 160
      63 Pro Pro Arg Asn Val Thr Leu Leu Gln Glu Arg Ala Asn Lys Leu Val
      64 165 170 175
      65 Lys Tyr Leu Met Ile Lys Asp Tyr Lys Lys Ile Pro Ile Lys Arg Ala
      66 180 185 190
      67 Asp Met Leu Lys Asp Val Ile Arg Glu Tyr Asp Glu His Phe Pro Glu
      68 195 200 205
      69 Ile Ile Glu Arg Ala Thr Tyr Thr Leu Glu Lys Lys Phe Gly Ile His
      70 210 215 220
      71 Leu Lys Glu Ile Asp Lys Glu Glu His Leu Tyr Ile Leu Val Cys Thr
      72 225 230 235 240
      73 Arg Asp Ser Ser Ala Arg Leu Leu Gly Lys Thr Lys Asp Thr Pro Arg
      74 245 250 255
      75 Leu Ser Leu Leu Leu Val Ile Leu Gly Val Ile Phe Met Asn Gly Asn
      76 260 265 270
      77 Arg Ala Ser Glu Ala Val Leu Trp Glu Ala Leu Arg Lys Met Gly Leu
      78 275 280 285
      79 Arg Pro Gly Val Arg His Pro Leu Leu Gly Asp Leu Arg Lys Leu Leu
      80 290 295 300
      81 Thr Tyr Glu Phe Val Lys Gln Lys Tyr Leu Asp Tyr Arg Arg Val Pro
      82 305 310 315 320
      83 Asn Ser Asn Pro Pro Glu Tyr Glu Phe Leu Trp Gly Leu Arg Ser Tyr
      84 325 330 335
      85 His Glu Thr Ser Lys Met Lys Val Leu Arg Phe Ile Ala Glu Val Gln
      86 340 345 350
      87 Lys Arg Asp Pro Arg Asp Trp Thr Ala Gln Phe Met Glu Ala Ala Asp
      88 355 360 365
      89 Glu Ala Leu Asp Ala Leu Asp Ala Ala Ala Glu Ala Glu Ala Arg
      90 370 375 380
      91 Ala Glu Ala Arg Thr Arg Met Gly Ile Gly Asp Glu Ala Val Ser Gly

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92 385          390          395          400
93 Pro Gly Ala Gly Met Thr Leu Ser Leu Ser Cys
94          405          410
96 (2) INFORMATION FOR SEQ ID NO: 2:
97   (i) SEQUENCE CHARACTERISTICS:
98       (A) LENGTH: 1247 base pairs
99       (B) TYPE: nucleic acid
100      (C) STRANDEDNESS: single
101      (D) TOPOLOGY: linear
102   (vii) IMMEDIATE SOURCE:
103       (A) LIBRARY: Consensus
104       (B) CLONE: Consensus
105   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
106 CNACGNGAAT GGCCTTCCCG CGCCCCAAGA AGAACCTGCC CCAGCCCAAG NAGGCTGCCA      60
107 CAGAGGGCCC CAGTGTCTGCC TCTGGTGTGC CCCAGACGGG ACCTGGCAGG GAGGTGGCAG      120
108 CCACCCGGCC CAAGACCACC AAGTCGGGGA AGGCGCTGGC CAAGACTCGG TGGGTGGAGC      180
109 CTCAGAATGT TGTGGCAGCA GCTGCTGCCA AGGCCAAGAT GGCCACGAGC ATCCCTGAGC      240
110 CGGAGGGTGC AGCTGCTGCC ACTGCTCAGC ACAGTGCTGA GCCCTGGGCC AGGATGGGAG      300
111 GCAAGAGGAC CAAGAAGTCC AAGCACCTGG ATGATGAGTA TGAGAGCAGC GAGGAGGAGA      360
112 GAGAGACTCC CGCGGTCCCA CCCACCTGGA GAGCATCACA GCCCTCATTG ACGGTGCGGG      420
113 CTCAGTTGGC CCCTCGGCCC CCGATGGCCC CGAGGTCCCA GATACCTCA AGGCACGTAC      480
114 TGTGCCTGCC CCCCCGCAAC GTGACCCCTC TGCAGGAGAG GGCAAATAAG TTGGTGAAAT      540
115 ACCTGATGAT TAAGGACTAC AAGAAGATCC CCATCAAGCG CGCAGACATG CTGAAGGATG      600
116 TCATCAGAGA ATATGATGAA CATTTCCTTG AGATCATTGA ACGAGCAACG TACACCCTGG      660
117 AAAAGAAGTT TGGGATCCAC CTGAAGGAGA TCGACAAGGA AGAACACCTG TATATTCTTG      720
118 TCTGCACACG GGAATCCTCA GCTCGCCTCC TTGGAAAAAC CAAGGACACT CCCAGGCTGA      780
119 GTCTCCTCTT GGTGATTCTG GCGTCATCT TCATGAATGG CAACCGTGCC AGCGAGGCTG      840
120 TCCTCTGGGA GGCATACGC AAGATGGGAC TCGTCCTGG GGTGAGACAT CCCCTCCTTG      900
121 GAGATCTAAG GAAACTTCTC ACCTATGAGT TTGTAAAGCA GAAATACCTG GACTACAGAC      960
122 GAGTGCCCAA CAGCAACCCC CCGGAGTATG AGTTCCTCTG GGGCCTCCGT TCCTACCATG      1020
123 AGACTAGCAA GATGAAAGTG CTGAGATTCA TTGCAGAGGT TCAGAAAAGA GACCCTCGTG      1080
124 ACTGGAATGC ACAGTTCATG GAGGCTGCAG ATGAGGCCTT GGATGCTCTG GATGAGGCTG      1140
125 CAGCTGAGGC CGAAGCCCGG GCTGAAGCAA GAACCCGCAT GGGAATTGGA GATGAGGCTG      1200
126 TGTCTGGGCC CGGAGCTGGG ATGACATTGA GTTTGAGCTG CTGACCT      1247
128 (2) INFORMATION FOR SEQ ID NO: 3:
129   (i) SEQUENCE CHARACTERISTICS:
130       (A) LENGTH: 347 amino acids
131       (B) TYPE: amino acid
132       (C) STRANDEDNESS: single
133       (D) TOPOLOGY: linear
134   (vii) IMMEDIATE SOURCE:
135       (A) LIBRARY: GenBank
136       (B) CLONE: 608993
137   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
138 Met Pro Arg Gly Gln Lys Ser Lys Leu Arg Ala Arg Glu Lys Arg Arg
139 1          5          10          15
140 Lys Ala Arg Glu Glu Thr Gln Gly Leu Lys Val Arg His Ala Thr Ala
141          20          25          30
142 Ala Glu Lys Glu Glu Cys Pro Ser Ser Ser Pro Val Leu Gly Asp Thr

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143          35          40          45
144 Pro Thr Ser Ser Pro Ala Ala Gly Ile Pro Gln Lys Pro Gln Gly Ala
145          50          55          60
146 Pro Pro Thr Thr Thr Ala Ala Ala Ala Val Ser Cys Thr Glu Ser Asp
147 65          70          75          80
148 Glu Gly Ala Lys Cys Gln Gly Glu Glu Asn Ala Ser Phe Ser Gln Ala
149          85          90          95
150 Thr Thr Ser Thr Glu Ser Ser Val Lys Asp Pro Val Ala Trp Glu Ala
151          100         105         110
152 Gly Met Leu Met His Phe Ile Leu Arg Lys Tyr Lys Met Arg Glu Pro
153          115         120         125
154 Ile Met Lys Ala Asp Met Leu Lys Val Val Asp Glu Lys Tyr Lys Asp
155          130         135         140
156 His Phe Thr Glu Ile Leu Asn Gly Ala Ser Arg Arg Leu Glu Leu Val
157 145          150          155          160
158 Phe Gly Leu Asp Leu Lys Glu Asp Asn Pro Ser Ser His Thr Tyr Thr
159          165         170         175
160 Leu Val Ser Lys Leu Asn Leu Thr Asn Asp Gly Asn Leu Ser Asn Asp
161          180         185         190
162 Trp Asp Phe Pro Arg Asn Gly Leu Leu Met Pro Leu Leu Gly Val Ile
163          195         200         205
164 Phe Leu Lys Gly Asn Ser Ala Thr Glu Glu Glu Ile Trp Lys Phe Met
165          210         215         220
166 Asn Val Leu Gly Ala Tyr Asp Gly Glu Glu His Leu Ile Tyr Gly Glu
167 225          230         235         240
168 Pro Arg Lys Phe Ile Thr Gln Asp Leu Val Gln Glu Lys Tyr Leu Lys
169          245         250         255
170 Tyr Glu Gln Val Pro Asn Ser Asp Pro Pro Arg Tyr Gln Phe Leu Trp
171          260         265         270
172 Gly Pro Arg Ala Tyr Ala Glu Thr Thr Lys Met Lys Val Leu Glu Phe
173          275         280         285
174 Leu Ala Lys Met Asn Gly Ala Thr Pro Arg Asp Phe Pro Ser His Tyr
175          290         295         300
176 Glu Glu Ala Leu Arg Asp Glu Glu Glu Arg Ala Gln Val Arg Ser Ser
177 305          310         315         320
178 Val Arg Ala Arg Arg Arg Thr Thr Ala Thr Thr Phe Arg Ala Arg Ser
179          325         330         335
180 Arg Ala Pro Phe Ser Arg Ser Ser His Pro Met
181          340         345

```

183 (2) INFORMATION FOR SEQ ID NO: 4:

184 (i) SEQUENCE CHARACTERISTICS:

185 (A) LENGTH: 369 amino acids

186 (B) TYPE: amino acid

187 (C) STRANDEDNESS: single

188 (D) TOPOLOGY: linear

189 (vii) IMMEDIATE SOURCE:

190 (A) LIBRARY: GenBank

191 (B) CLONE: 533511

192 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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```

193 Met Pro Arg Ala Pro Lys Arg Gln Arg Cys Met Pro Glu Glu Asp Leu
194 1 5 10 15
195 Gln Ser Gln Ser Glu Thr Gln Gly Leu Glu Gly Ala Gln Ala Pro Leu
196 20 25 30
197 Ala Val Glu Asp Ala Ser Ser Ser Thr Ser Thr Ser Ser Ser Phe
198 35 40 45
199 Pro Ser Ser Phe Pro Ser Ser Ser Ser Ser Ser Ser Ser Cys Tyr
200 50 55 60
201 Pro Leu Ile Pro Ser Thr Pro Glu Glu Val Ser Ala Asp Asp Glu Thr
202 65 70 75 80
203 Pro Asn Pro Pro Gln Ser Ala Gln Ile Ala Cys Ser Ser Pro Ser Val
204 85 90 95
205 Val Ala Ser Leu Pro Leu Asp Gln Ser Asp Glu Gly Ser Ser Gln
206 100 105 110
207 Lys Glu Glu Ser Pro Ser Thr Leu Gln Val Leu Pro Asp Ser Glu Ser
208 115 120 125
209 Leu Pro Arg Ser Glu Ile Asp Glu Lys Val Thr Asp Leu Val Gln Phe
210 130 135 140
211 Leu Leu Phe Lys Tyr Gln Met Lys Glu Pro Ile Thr Lys Ala Glu Ile
212 145 150 155 160
213 Leu Glu Ser Val Ile Lys Asn Tyr Glu Asp His Phe Pro Leu Leu Phe
214 165 170 175
215 Ser Glu Ala Ser Glu Cys Met Leu Leu Val Phe Gly Ile Asp Val Lys
216 180 185 190
217 Glu Val Asp Pro Thr Gly His Ser Phe Val Leu Val Thr Ser Leu Gly
218 195 200 205
219 Leu Thr Tyr Asp Gly Met Leu Ser Asp Val Gln Ser Met Pro Lys Thr
220 210 215 220
221 Gly Ile Leu Ile Leu Ile Leu Ser Ile Ile Phe Ile Glu Gly Tyr Cys
222 225 230 235 240
223 Thr Pro Glu Glu Val Ile Trp Glu Ala Leu Asn Met Met Gly Leu Tyr
224 245 250 255
225 Asp Gly Met Glu His Leu Ile Tyr Gly Glu Pro Arg Lys Leu Leu Thr
226 260 265 270
227 Gln Asp Trp Val Gln Glu Asn Tyr Leu Glu Tyr Arg Gln Val Pro Gly
228 275 280 285
229 Ser Asp Pro Ala Arg Tyr Glu Phe Leu Trp Gly Pro Arg Ala His Ala
230 290 295 300
231 Glu Ile Arg Lys Met Ser Leu Leu Lys Phe Leu Ala Lys Val Asn Gly
232 305 310 315 320
233 Ser Asp Pro Arg Ser Phe Pro Leu Trp Tyr Glu Glu Ala Leu Lys Asp
234 325 330 335
235 Glu Glu Glu Arg Ala Gln Asp Arg Ile Ala Thr Thr Asp Asp Thr Thr
236 340 345 350
237 Ala Met Ala Ser Ala Ser Ser Ser Ala Thr Gly Ser Phe Ser Tyr Pro
238 355 360 365
239 Glu
241 (2) INFORMATION FOR SEQ ID NO: 5:
242 (i) SEQUENCE CHARACTERISTICS:

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